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 McBride, Jere W.
 Yu, Xue-Jie

<120> Homologous 28-Kilodalton Immunodominant Protein
 Genes of *Ehrlichia canis* and Uses Thereof

<130> D6152CIP2/D1/D

<141> 2003-10-07

<150> 10/062,624
 <151> 2002-01-31

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<220>
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aacatgattg	ggatggaagt	ccaatactta	agaataaaca	cgctgacttt	400
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tgcaggagct	atcggttact	caatgggtgg	ccaagaata	gaattcgaaa	500
tatcttatga	agcattcgac	gtaaaaagtc	ctaatatcaa	ttatcaaaat	550
gacgcgcaca	ggtactgcgc	tctatctcat	cacacatcgg	cagccatgga	600
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Asp	Glu	Ile	Val	Gly	Pro	Gln	Phe	Ala	Thr	Val	Thr	Leu	Asn	Val
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Cys	Tyr	Phe	Gly	Leu	Glu	Leu	Gly	Cys	Arg	Phe	Asn	Phe		
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 agaacggcgc acacagatac tgtgctttat ctcatcatag ttcagcaaca 450
 agcatgtcct ccgcaagtaa caaatttggt ttcttaaaaa atgaagggtt 500
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 attaggttat agtataagtt cagaagcctc tgtttttatc ggtggacact 700
 ttcacagagt cataggtaat gaatttagag acatccctgc tatggttcct 750
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 <213> *Ehrlichia canis*

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 Asp Asn Thr Gly Ser Phe Tyr Ile Ser Gly Lys Tyr Val Pro Ser
 35 40 45
 Val Ser His Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Ser
 50 55 60
 Thr Val Gly Val Phe Gly Leu Lys His Asp Trp Asn Gly Gly Thr
 65 70 75
 Ile Ser Asn Ser Ser Pro Glu Asn Ile Phe Thr Val Gln Asn Tyr
 80 85 90
 Ser Phe Lys Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala
 95 100 105
 Ile Gly Tyr Ser Met Gly Gly Pro Arg Ile Glu Leu Glu Val Leu
 110 115 120
 Tyr Glu Thr Phe Asp Val Lys Asn Gln Asn Asn Asn Tyr Lys Asn
 125 130 135
 Gly Ala His Arg Tyr Cys Ala Leu Ser His His Ser Ser Ala Thr
 140 145 150
 Ser Met Ser Ser Ala Ser Asn Lys Phe Val Phe Leu Lys Asn Glu
 155 160 165
 Gly Leu Ile Asp Leu Ser Phe Met Ile Asn Ala Cys Tyr Asp Ile
 170 175 180
 Ile Ile Glu Gly Met Pro Phe Ser Pro Tyr Ile Cys Ala Gly Val
 185 190 195

Gly	Thr	Asp	Val	Val	Ser	Met	Phe	Glu	Ala	Ile	Asn	Pro	Lys	Ile
				200					205					210
Ser	Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Gly	Tyr	Ser	Ile	Ser	Ser	Glu
				215					220					225
Ala	Ser	Val	Phe	Ile	Gly	Gly	His	Phe	His	Arg	Val	Ile	Gly	Asn
				230					235					240
Glu	Phe	Arg	Asp	Ile	Pro	Ala	Met	Val	Pro	Ser	Gly	Ser	Asn	Leu
				245					250					255
Pro	Glu	Asn	Gln	Phe	Ala	Ile	Val	Thr	Leu	Asn	Val	Cys	His	Phe
				260					265					270
Gly	Ile	Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe					
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 <213> *Ehrlichia canis*

<220>
 <223> partial amino acid sequence of p28-5 protein

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Ile	Tyr	Phe	Leu	Pro	Asn	Val	Ser	Tyr	Ser	Asn	Pro	Val	Tyr	Gly
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Asn	Ser	Met	Tyr	Gly	Asn	Phe	Tyr	Ile	Ser	Gly	Lys	Tyr	Met	Pro
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Ser	Val	Pro	His	Phe	Gly	Ile	Phe	Ser	Ala	Glu	Glu	Glu	Lys	Lys
				50					55					60
Lys	Thr	Thr	Val	Val	Tyr	Gly	Leu	Lys	Glu	Asn	Trp	Ala	Gly	Asp
				65					70					75
Ala	Ile	Ser	Ser	Gln	Ser	Pro	Asp	Asp	Asn	Phe	Thr	Ile	Arg	Asn
				80					85					90

Tyr	Ser	Phe	Lys	Tyr	Ala	Ser	Asn	Lys	Phe	Leu	Gly	Phe	Ala	Val
				95					100					105
Ala	Ile	Gly	Tyr	Ser	Ile	Gly	Ser	Pro	Arg	Ile	Glu	Val	Glu	Met
				110					115					120
Ser	Tyr	Glu	Ala	Phe	Asp	Val	Lys	Asn	Gln	Gly	Asn	Asn		
				125					130					

<210> 8
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 <212> PRT
 <213> *Ehrlichia canis*

<220>
 <223> amino acid sequence of p28-4 protien

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Thr	Ser	Phe	Thr	His	Phe	Ile	Pro	Phe	Tyr	Ser	Pro	Ala	Arg	Ala
				20					25					30
Ser	Thr	Ile	His	Asn	Phe	Tyr	Ile	Ser	Gly	Lys	Tyr	Met	Pro	Thr
				35					40					45
Ala	Ser	His	Phe	Gly	Ile	Phe	Ser	Ala	Lys	Glu	Glu	Gln	Ser	Phe
				50					55					60
Thr	Lys	Val	Leu	Val	Gly	Leu	Asp	Gln	Arg	Leu	Ser	His	Asn	Ile
				65					70					75
Ile	Asn	Asn	Asn	Asp	Thr	Ala	Lys	Ser	Leu	Lys	Val	Gln	Asn	Tyr
				80					85					90
Ser	Phe	Lys	Tyr	Lys	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Ala
				95					100					105
Ile	Gly	Tyr	Ser	Ile	Gly	Asn	Ser	Arg	Ile	Glu	Leu	Glu	Val	Ser
				110					115					120
His	Glu	Ile	Phe	Asp	Thr	Lys	Asn	Pro	Gly	Asn	Asn	Tyr	Leu	Asn
				125					130					135

Asp	Ser	His	Lys	Tyr	Cys	Ala	Leu	Ser	His	Gly	Ser	His	Ile	Cys	
				140					145					150	
Ser	Asp	Gly	Asn	Ser	Gly	Asp	Trp	Tyr	Thr	Ala	Lys	Thr	Asp	Lys	
				155					160					165	
Phe	Val	Leu	Leu	Lys	Asn	Glu	Gly	Leu	Leu	Asp	Val	Ser	Phe	Met	
				170					175					180	
Leu	Asn	Ala	Cys	Tyr	Asp	Ile	Thr	Thr	Glu	Lys	Met	Pro	Phe	Ser	
				185					190					195	
Pro	Tyr	Ile	Cys	Ala	Gly	Ile	Gly	Thr	Asp	Leu	Ile	Ser	Met	Phe	
				200					205					210	
Glu	Thr	Thr	Gln	Asn	Lys	Ile	Ser	Tyr	Gln	Gly	Lys	Leu	Gly	Leu	
				215					220					225	
Asn	Tyr	Thr	Ile	Asn	Ser	Arg	Val	Ser	Val	Phe	Ala	Gly	Gly	His	
				230					235					240	
Phe	His	Lys	Val	Ile	Gly	Asn	Glu	Phe	Lys	Gly	Ile	Pro	Thr	Leu	
				245					250					255	
Leu	Pro	Asp	Gly	Ser	Asn	Ile	Lys	Val	Gln	Gln	Ser	Ala	Thr	Val	
				260					265					270	
Thr	Leu	Asp	Val	Cys	His	Phe	Gly	Leu	Glu	Ile	Gly	Ser	Arg	Phe	
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Phe	Phe														

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<211> 281

<212> PRT

<213> *Ehrlichia chaffeensis*

<220>

<223> amino acid sequence of *E. chaffeensis* P28

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Gly	Ile	Asn	Gly	Asn	Phe	Tyr	Ile	Ser	Gly	Lys	Tyr	Met	Pro	Ser	35	40	45
Ala	Ser	His	Phe	Gly	Val	Phe	Ser	Ala	Lys	Glu	Glu	Arg	Asn	Thr	50	55	60
Thr	Val	Gly	Val	Phe	Gly	Leu	Lys	Gln	Asn	Trp	Asp	Gly	Ser	Ala	65	70	75
Ile	Ser	Asn	Ser	Ser	Pro	Asn	Asp	Val	Phe	Thr	Val	Ser	Asn	Tyr	80	85	90
Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Ala	95	100	105
Ile	Gly	Tyr	Ser	Met	Asp	Gly	Pro	Arg	Ile	Glu	Leu	Glu	Val	Ser	110	115	120
Tyr	Glu	Thr	Phe	Asp	Val	Lys	Asn	Gln	Gly	Asn	Asn	Tyr	Lys	Asn	125	130	135
Glu	Ala	His	Arg	Tyr	Cys	Ala	Leu	Ser	His	Asn	Ser	Ala	Ala	Asp	140	145	150
Met	Ser	Ser	Ala	Ser	Asn	Asn	Phe	Val	Phe	Leu	Lys	Asn	Glu	Gly	155	160	165
Leu	Leu	Asp	Ile	Ser	Phe	Met	Leu	Asn	Ala	Cys	Tyr	Asp	Val	Val	170	175	180
Gly	Glu	Gly	Ile	Pro	Phe	Ser	Pro	Tyr	Ile	Cys	Ala	Gly	Ile	Gly	185	190	195
Thr	Asp	Leu	Val	Ser	Met	Phe	Glu	Ala	Thr	Asn	Pro	Lys	Ile	Ser	200	205	210
Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Ser	Ile	Ser	Pro	Glu	Ala	215	220	225
Ser	Val	Phe	Ile	Gly	Gly	His	Phe	His	Lys	Val	Ile	Gly	Asn	Glu	230	235	240
Phe	Arg	Asp	Ile	Pro	Thr	Ile	Ile	Pro	Thr	Gly	Ser	Thr	Leu	Ala	245	250	255
Gly	Lys	Gly	Asn	Tyr	Pro	Ala	Ile	Val	Ile	Leu	Asp	Val	Cys	His	260	265	270

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<210> 10

<211> 283

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<213> *Ehrlichia chaffeensis*

<220>

<223> amino acid sequence of *E. chaffeensis* OMP-1B

<400> 10

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				20					25					30
Asn	Asp	Thr	Gly	Ile	Asn	Asp	Ser	Arg	Glu	Gly	Phe	Tyr	Ile	Ser
				35					40					45
Val	Lys	Tyr	Asn	Pro	Ser	Ile	Ser	His	Phe	Arg	Lys	Phe	Ser	Ala
				50					55					60
Glu	Glu	Ala	Pro	Ile	Asn	Gly	Asn	Thr	Ser	Ile	Thr	Lys	Lys	Val
				65					70					75
Phe	Gly	Leu	Lys	Lys	Asp	Gly	Asp	Ile	Ala	Gln	Ser	Ala	Asn	Phe
				80					85					90
Asn	Arg	Thr	Asp	Pro	Ala	Leu	Glu	Phe	Gln	Asn	Asn	Leu	Ile	Ser
				95					100					105
Gly	Phe	Ser	Gly	Ser	Ile	Gly	Tyr	Ala	Met	Asp	Gly	Pro	Arg	Ile
				110					115					120
Glu	Leu	Glu	Ala	Ala	Tyr	Gln	Lys	Phe	Asp	Ala	Lys	Asn	Pro	Asp
				125					130					135
Asn	Asn	Asp	Thr	Asn	Ser	Gly	Asp	Tyr	Tyr	Lys	Tyr	Phe	Gly	Leu
				140					145					150
Ser	Arg	Glu	Asp	Ala	Ile	Ala	Asp	Lys	Lys	Tyr	Val	Val	Leu	Lys
				155					160					165

Asn	Glu	Gly	Ile	Thr	Phe	Met	Ser	Leu	Met	Val	Asn	Thr	Cys	Tyr
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Asp	Ile	Thr	Ala	Glu	Gly	Val	Pro	Phe	Ile	Pro	Tyr	Ala	Cys	Ala
				185					190					195
Gly	Val	Gly	Ala	Asp	Leu	Ile	Asn	Val	Phe	Lys	Asp	Phe	Asn	Leu
				200					205					210
Lys	Phe	Ser	Tyr	Gln	Gly	Lys	Ile	Gly	Ile	Ser	Tyr	Pro	Ile	Thr
				215					220					225
Pro	Glu	Val	Ser	Ala	Phe	Ile	Gly	Gly	Tyr	Tyr	His	Gly	Val	Ile
				230					235					240
Gly	Asn	Asn	Phe	Asn	Lys	Ile	Pro	Val	Ile	Thr	Pro	Val	Val	Leu
				245					250					255
Glu	Gly	Ala	Pro	Gln	Thr	Thr	Ser	Ala	Leu	Val	Thr	Ile	Asp	Thr
				260					265					270
Gly	Tyr	Phe	Gly	Gly	Glu	Val	Gly	Val	Arg	Phe	Thr	Phe		
				275					280					

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<211> 280

<212> PRT

<213> *Ehrlichia chaffeensis*

<220>

<223> amino acid sequence of *E. chaffeensis* OMP-1C

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				20					25					30
Asp	Ser	Val	Ser	Gly	Asn	Phe	Tyr	Ile	Ser	Gly	Lys	Tyr	Met	Pro
				35					40					45
Ser	Ala	Ser	His	Phe	Gly	Val	Phe	Ser	Ala	Lys	Glu	Glu	Lys	Asn
				50					55					60

Pro	Thr	Val	Ala	Leu	Tyr	Gly	Leu	Lys	Gln	Asp	Trp	Asn	Gly	Val	65	70	75
Ser	Ala	Ser	Ser	His	Ala	Asp	Ala	Asp	Phe	Asn	Asn	Lys	Gly	Tyr	80	85	90
Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Ala	95	100	105
Ile	Gly	Tyr	Ser	Met	Gly	Gly	Pro	Arg	Ile	Glu	Phe	Glu	Val	Ser	110	115	120
Tyr	Glu	Thr	Phe	Asp	Val	Lys	Asn	Gln	Gly	Gly	Asn	Tyr	Lys	Asn	125	130	135
Asp	Ala	His	Arg	Tyr	Cys	Ala	Leu	Asp	Arg	Lys	Ala	Ser	Ser	Thr	140	145	150
Asn	Ala	Thr	Ala	Ser	His	Tyr	Val	Leu	Leu	Lys	Asn	Glu	Gly	Leu	155	160	165
Leu	Asp	Ile	Ser	Leu	Met	Leu	Asn	Ala	Cys	Tyr	Asp	Val	Val	Ser	170	175	180
Glu	Gly	Ile	Pro	Phe	Ser	Pro	Tyr	Ile	Cys	Ala	Gly	Val	Gly	Thr	185	190	195
Asp	Leu	Ile	Ser	Met	Phe	Glu	Ala	Ile	Asn	Pro	Lys	Ile	Ser	Tyr	200	205	210
Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Ser	Ile	Asn	Pro	Glu	Ala	Ser	215	220	225
Val	Phe	Val	Gly	Gly	His	Phe	His	Lys	Val	Ala	Gly	Asn	Glu	Phe	230	235	240
Arg	Asp	Ile	Ser	Thr	Leu	Lys	Ala	Phe	Ala	Thr	Pro	Ser	Ser	Ala	245	250	255
Ala	Thr	Pro	Asp	Leu	Ala	Thr	Val	Thr	Leu	Ser	Val	Cys	His	Phe	260	265	270
Gly	Val	Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe						275	280	

<210> 12
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<213> *Ehrlichia chaffeensis*

<220>

<223> amino acid sequence of *E. chaffeensis* OMP-1D

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Asp Asn Ile Ser Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro
              35              40              45
Ser Ala Ser His Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn
              50              55              60
Thr Thr Val Gly Val Phe Gly Ile Glu Gln Asp Trp Asp Arg Cys
              65              70              75
Val Ile Ser Arg Thr Thr Leu Ser Asp Ile Phe Thr Val Pro Asn
              80              85              90
Tyr Ser Phe Lys Tyr Glu Asn Asn Leu Phe Ser Gly Phe Ala Gly
              95              100             105
Ala Ile Gly Tyr Ser Met Asp Gly Pro Arg Ile Glu Leu Glu Val
              110             115             120
Ser Tyr Glu Ala Phe Asp Val Lys Asn Gln Gly Asn Asn Tyr Lys
              125             130             135
Asn Glu Ala His Arg Tyr Tyr Ala Leu Ser His Leu Leu Gly Thr
              140             145             150
Glu Thr Gln Ile Asp Gly Ala Gly Ser Ala Ser Val Phe Leu Ile
              155             160             165
Asn Glu Gly Leu Leu Asp Lys Ser Phe Met Leu Asn Ala Cys Tyr
              170             175             180
Asp Val Ile Ser Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys Ala
              185             190             195
Gly Ile Gly Ile Asp Leu Val Ser Met Phe Glu Ala Ile Asn Pro
              200             205             210
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Lys	Ile	Ser	Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Pro	Ile	Ser
				215					220					225
Pro	Glu	Ala	Ser	Val	Phe	Ile	Gly	Gly	His	Phe	His	Lys	Val	Ile
				230					235					240
Gly	Asn	Glu	Phe	Arg	Asp	Ile	Pro	Thr	Met	Ile	Pro	Ser	Glu	Ser
				245					250					255
Ala	Leu	Ala	Gly	Lys	Gly	Asn	Tyr	Pro	Ala	Ile	Val	Thr	Leu	Asp
				260					265					270
Val	Phe	Tyr	Phe	Gly	Ile	Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe	Gln
				275					280					285
Leu														

<210> 13
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 <213> *Ehrlichia chaffeensis*

<220>
 <223> amino acid sequence of *E. chaffeensis* OMP-1E

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Met	Ser	Phe	Leu	Pro	Gly	Ile	Ser	Phe	Ser	Asp	Pro	Val	Gln	Gly
				20					25					30
Asp	Asn	Ile	Ser	Gly	Asn	Phe	Tyr	Val	Ser	Gly	Lys	Tyr	Met	Pro
				35					40					45
Ser	Ala	Ser	His	Phe	Gly	Met	Phe	Ser	Ala	Lys	Glu	Glu	Lys	Asn
				50					55					60
Pro	Thr	Val	Ala	Leu	Tyr	Gly	Leu	Lys	Gln	Asp	Trp	Glu	Gly	Ile
				65					70					75
Ser	Ser	Ser	Ser	His	Asn	Asp	Asn	His	Phe	Asn	Asn	Lys	Gly	Tyr
				80					85					90
Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Ala
				95					100					105

Ile Gly Tyr Ser Met Gly Gly Pro Arg Val Glu Phe Glu Val Ser		
	110	115 120
Tyr Glu Thr Phe Asp Val Lys Asn Gln Gly Asn Asn Tyr Lys Asn		
	125	130 135
Asp Ala His Arg Tyr Cys Ala Leu Gly Gln Gln Asp Asn Ser Gly		
	140	145 150
Ile Pro Lys Thr Ser Lys Tyr Val Leu Leu Lys Ser Glu Gly Leu		
	155	160 165
Leu Asp Ile Ser Phe Met Leu Asn Ala Cys Tyr Asp Ile Ile Asn		
	170	175 180
Glu Ser Ile Pro Leu Ser Pro Tyr Ile Cys Ala Gly Val Gly Thr		
	185	190 195
Asp Leu Ile Ser Met Phe Glu Ala Thr Asn Pro Lys Ile Ser Tyr		
	200	205 210
Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Asn Pro Glu Ala Ser		
	215	220 225
Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn Glu Phe		
	230	235 240
Arg Asp Ile Pro Thr Leu Lys Ala Phe Val Thr Ser Ser Ala Thr		
	245	250 255
Pro Asp Leu Ala Ile Val Thr Leu Ser Val Cys His Phe Gly Ile		
	260	265 270
Glu Leu Gly Gly Arg Phe Asn Phe		
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<211> 280

<212> PRT

<213> *Ehrlichia chaffeensis*

<220>

<223> amino acid sequence of *E. chaffeensis* OMP-1F

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	20	25 30
Asp Asn Val Gly	Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Val Pro	
	35	40 45
Ser Val Ser His	Phe Gly Val Phe Ser Ala Lys Gln Glu Arg Asn	
	50	55 60
Thr Thr Thr Gly	Val Phe Gly Leu Lys Gln Asp Trp Asp Gly Ser	
	65	70 75
Thr Ile Ser Lys	Asn Ser Pro Glu Asn Thr Phe Asn Val Pro Asn	
	80	85 90
Tyr Ser Phe Lys	Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly	
	95	100 105
Ala Val Gly Tyr	Leu Met Asn Gly Pro Arg Ile Glu Leu Glu Met	
	110	115 120
Ser Tyr Glu Thr	Phe Asp Val Lys Asn Gln Gly Asn Asn Tyr Lys	
	125	130 135
Asn Asp Ala His	Lys Tyr Tyr Ala Leu Thr His Asn Ser Gly Gly	
	140	145 150
Lys Leu Ser Asn	Ala Gly Asp Lys Phe Val Phe Leu Lys Asn Glu	
	155	160 165
Gly Leu Leu Asp	Ile Ser Leu Met Leu Asn Ala Cys Tyr Asp Val	
	170	175 180
Ile Ser Glu Gly	Ile Pro Phe Ser Pro Tyr Ile Cys Ala Gly Val	
	185	190 195
Gly Thr Asp Leu	Ile Ser Met Phe Glu Ala Ile Asn Pro Lys Ile	
	200	205 210
Ser Tyr Gln Gly	Lys Leu Gly Leu Ser Tyr Ser Ile Ser Pro Glu	
	215	220 225
Ala Ser Val Phe	Val Gly Gly His Phe His Lys Val Ile Gly Asn	
	230	235 240
Glu Phe Arg Asp	Ile Pro Ala Met Ile Pro Ser Thr Ser Thr Leu	
	245	250 255

Thr	Gly	Asn	His	Phe	Thr	Ile	Val	Thr	Leu	Ser	Val	Cys	His	Phe
				260					265					270
Gly	Val	Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe					
				275					280					

<210> 15
 <211> 284
 <212> PRT
 <213> *Cowdria ruminantium*

<220>
 <223> amino acid sequence of *C. ruminantium* MAP-1

<400>				15										
Met	Asn	Cys	Lys	Lys	Ile	Phe	Ile	Thr	Ser	Thr	Leu	Ile	Ser	Leu
				5					10					15
Val	Ser	Phe	Leu	Pro	Gly	Val	Ser	Phe	Ser	Asp	Val	Ile	Gln	Glu
				20					25					30
Glu	Asn	Asn	Pro	Val	Gly	Ser	Val	Tyr	Ile	Ser	Ala	Lys	Tyr	Met
				35					40					45
Pro	Thr	Ala	Ser	His	Phe	Gly	Lys	Met	Ser	Ile	Lys	Glu	Asp	Ser
				50					55					60
Arg	Asp	Thr	Lys	Ala	Val	Phe	Gly	Leu	Lys	Lys	Asp	Trp	Asp	Gly
				65					70					75
Val	Lys	Thr	Pro	Ser	Gly	Asn	Thr	Asn	Ser	Ile	Phe	Thr	Glu	Lys
				80					85					90
Asp	Tyr	Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala
				95					100					105
Gly	Ala	Val	Gly	Tyr	Ser	Met	Asn	Gly	Pro	Arg	Ile	Glu	Phe	Glu
				110					115					120
Val	Ser	Tyr	Glu	Thr	Phe	Asp	Val	Arg	Asn	Pro	Gly	Gly	Asn	Tyr
				125					130					135
Lys	Asn	Asp	Ala	His	Met	Tyr	Cys	Ala	Leu	Asp	Thr	Ala	Ser	Ser
				140					145					150

Ser Thr Ala Gly Ala Thr Thr Ser Val Met Val Lys Asn Glu Asn		
	155	160 165
Leu Thr Asp Ile Ser Leu Met Leu Asn Ala Cys Tyr Asp Ile Met		
	170	175 180
Leu Asp Gly Met Pro Val Ser Pro Tyr Val Cys Ala Gly Ile Gly		
	185	190 195
Thr Asp Leu Val Ser Val Ile Asn Ala Thr Asn Pro Lys Leu Ser		
	200	205 210
Tyr Gln Gly Lys Leu Gly Ile Ser Tyr Ser Ile Asn Pro Glu Ala		
	215	220 225
Ser Ile Phe Ile Gly Gly His Phe His Arg Val Ile Gly Asn Glu		
	230	235 240
Phe Lys Asp Ile Ala Thr Ser Lys Val Phe Thr Ser Ser Gly Asn		
	245	250 255
Ala Ser Ser Ala Val Ser Pro Gly Phe Ala Ser Ala Ile Leu Asp		
	260	265 270
Val Cys His Phe Gly Ile Glu Ile Gly Gly Arg Phe Val Phe		
	275	280

<210> 16
 <211> 20
 <212> DNA
 <213> artificial sequence

<220>
 <221> primer_bind
 <222> nucleotides 313-332 of *C. ruminantium* MAP-1,
 also nucleotides 307-326 of *E. chaffeensis* P28
 <223> forward primer 793 for PCR

<400> 16
 gcaggagctg ttggttactc 20

<210> 17
 <211> 21
 <212> DNA
 <213> artificial sequence

 <220>
 <221> primer_bind
 <222> nucleotides 823-843 of *C. ruminantium* MAP-1,
 also nucleotides 814-834 of *E. chaffeensis* P28
 <223> reverse primer 1330 for PCR

<400> 17
 ccttcctcca agttctatgc c 21

<210> 18
 <211> 24
 <212> DNA
 <213> artificial sequence

 <220>
 <221> primer_bind
 <223> primer 46f, specific for *p28-5* gene

<400> 18
 atatacttcc tacctaattgt ctca 24

<210> 19
 <211> 20
 <212> DNA
 <213> artificial sequence

 <220>
 <221> primer_bind

<223> primer used for sequencing 28-kDa protein
 genes in *E. canis*

<400> 19
 agtgcagagt cttcggtttc 20

<210> 20
 <211> 18
 <212> DNA
 <213> artificial sequence

<220>
 <221> primer_bind
 <223> primer used for sequencing 28-kDa protein
 genes in *E. canis*

<400> 20
 gttacttgcg gaggacat 18

<210> 21
 <211> 24
 <212> DNA
 <213> artificial sequence

<220>
 <221> primer_bind
 <222> nucleotides 687-710 of *E. canis* p28-7
 <223> primer 394 for PCR

<400> 21
 gcatttccac aggatcatag gtaa 24

<210>	22	
<211>	24	
<212>	DNA	
<213>	artificial sequence	
<220>		
<221>	primer_bind	
<222>	nucleotides 710-687 of <i>E. canis p28-7</i>	
<223>	primer 394C for PCR	
<400>	22	
ttacctatga	tcctgtggaa	atgc 24
<210>	23	
<211>	20	
<212>	DNA	
<213>	artificial sequence	
<220>		
<221>	primer_bind	
<223>	primer 793C which anneals to a region with <i>E. canis p28-7</i> , used to amplify the intergenic region between gene <i>p28-6</i> and <i>p28-7</i>	
<400>	23	
gagtaaccaa	cagctcctgc	20
<210>	24	
<211>	24	
<212>	DNA	
<213>	artificial sequence	
<220>		
<221>	primer_bind	

<222>
 <223> primer EC280M-F complementary to noncoding regions
 adjacent to the open reading frame of *p28-7*

 <400> 24
 tctacttttgc acttccacta ttgt 24

 <210> 25
 <211> 24
 <212> DNA
 <213> artificial sequence

 <220>
 <221> primer_bind
 <222>
 <223> primer EC280M-R complementary to noncoding regions
 adjacent to the open reading frame of *p28-7*

 <400> 25
 attctttttgc cactattttt cttt 24

 <210> 26
 <211> 25
 <212> DNA
 <213> artificial sequence

 <220>
 <221> primer_bind
 <223> primer *ECaSA3-2* corresponding to regions within
p28-6, used to amplify the intergenic region NC3
 between gene *p28-6* and *p28-7*

 <400> 26
 ctaggattag gttatagtat aagtt 25

<210> 27

<211> 23

<212> PRT

<213> *Ehrlichia canis*

<220>

<221> PEPTIDE

<223> a predicted N-terminal signal peptide of p28-7
and p28-6

<400> 27

Met Asn Cys Lys Lys Ile Leu Ile Thr Thr Ala Leu Met Ser Leu

5

10

15

Met Tyr Tyr Ala Pro Ser Ile Ser

20

<210> 28

<211> 25

<212> PRT

<213> *Ehrlichia chaffeensis*

<220>

<223> amino acid sequence of N-terminal signal peptide of
E. chaffeensis P28

<400> 28

Met Asn Tyr Lys Lys Ile Leu Ile Thr Ser Ala Leu Ile Ser Leu

5

10

15

Ile Ser Ser Leu Pro Gly Val Ser Phe Ser

20

25

<210> 29

<211> 26

<212> PRT

<213> *Ehrlichia canis*

<220>

<223> amino acid sequence of putative cleavage site of
p28-7

<400> 29

Met Asn Cys Lys Lys Ile Leu Ile Thr Thr Ala Leu Ile Ser Leu

5

10

15

Met Tyr Ser Ile Pro Ser Ile Ser Ser Phe Ser

20

25

<210> 30

<211> 299

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of intergenic
noncoding region 1 (28NC1)

<400> 30

taatacttct attgtacatg ttaaaaatag tactagtttg cttctgtggt 50

ttataaacgc aagagagaaa tagttagtaa taaattagaa agttaaatat 100

tagaaaagtc atatgttttt cattgtcatt gatactcaac taaaagtagt 150

ataaatgtta cttattaata attttacgta gtatattaaa tttcccttac 200

aaaagccact agtatatttat actaaaagct atactttggc ttgtatttaa 250

tttgtatttt tactactgtt aatttacttt cactgtttct ggtgtaaat 299

<210> 31

<211> 345

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of intergenic noncoding
region 2 (28NC2)

<400> 31

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taatttcgtg gtacacatat cacgaagcta aaattgtttt tttatctctg 50
ctgtatacaa gagaaaaaat agtagtgaaa attacctaac aatatgacag 100
tacaagttta ccaagcttat tctcacaaaa cttcttgtgt cttttatctc 150
tttacaatga aatgtacact tagcttcact actgtagagt gtgtttatca 200
atgctttgtt tattaatact ctacataata tgttaaattt ttcttacaaa 250
actcactagt aattttatact agaatatata ttctgacttg tatttgcttt 300
atacttccac tattgttaat ttattttcac tatttttaggt gtaat      345
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<210> 32

<211> 345

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of intergenic
noncoding region 3 (28NC3)

<400> 32

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tgatttttatt gttgccacat attaaaaatg atctaaactt gtttttatta 50
ttgctacata caaaaaaaag aaaaatagtg gcaaaagaat gtagcaataa 100
gaggggggggg ggggactaaa tttaccttct attcttctaa tattctttac 150
tatattcaaa tagcacaact caatgcttcc aggaaaatat gtttctaata 200
ttttatttat taccaatcct tatataatat attaaatttc tcttacaaaa 250
atctctaatag ttttatactt aatatatata ttctggcttg tatttacttt 300
gcacttccac tattgttaat ttattttcac tatttttaggt gtaat      345
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<210> 33

<211> 355

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of intergenic
noncoding region 4 (28NC4)

<400> 33

```
taattttatt gttgccacat attaaaaatg atctaaactt gtttttawta 50
ttgctacata caaaaaaaga aaaatagtgg caaaagaatg tagcaataag 100
aggggggggg gggaccaaat ttatcttcta tgcttcccaa gttttttcyc 150
gctatttatg acttaaacia cagaaggtaa ttccttcacg gaaaacttat 200
cttcaaatat tttatttatt accaatctta tataatatat taaatttctc 250
ttacaaaaat cactagtatt ttataccaaa atatattatc tgacttgctt 300
ttcttctgca cttctactat ttttaattta tttgtcacta ttaggttata 350
ataaw                                             355
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<210> 34

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> primer p28-5-818f

<400> 34

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ttaaacaatat gccacttcgg acta           24
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<210> 35

<211> 28

<212> DNA

<213> artificial sequence

<220>

<223> primer 1191

<400> 35
tatgatcgtg taaaattgct gtgagtat 28

<210> 36
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> primer ECa28-75C

<400> 36
tactggcacg tgctggacta 20

<210> 37
<211> 22
<212> DNA
<213> artificial sequence

<220>
<223> primer ECa5'-1600

<400> 37
caccaataaa tgcagagact tc 22

<210> 38
<211> 26
<212> DNA
<213> artificial sequence

<220>
<223> primer 3125

<400> 38
aatccatcat ttctcattac agtgtg 26

<210> 39

<211> 879

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of *E. canis* p28-1

<400> 39
atgaataata aactcaaatt tactataata aacacagtat tagtatgctt 50
attgtcatta cctaataatat cttcctcaaa ggccataaac aataacgcta 100
aaaagtacta cggattatat atcagtggac aatataaacc cagtgtttct 150
gttttcagta atttttcagt taaagaaacc aatgtcataa ctaaaaacct 200
tatagcttta aaaaaagatg ttgactctat tgaaaccaag actgatgcc 250
gtgtaggtat tagtaacca tcaaatttta ctatccccta tacagctgta 300
tttcaagata attctgtcaa tttcaatgga actattgggt acacctttgc 350
tgaaggtaca agagttgaaa tagaagggtc ttatgaggaa tttgatgtta 400
aaaaccctgg aggctataca ctaagtgatg cctatcgcta ttttgcatta 450
gcacgtgaaa tgaaaggtaa tagttttaca cctaaagaaa aagtttctaa 500
tagtatTTTTT cactctgtaa tgagaaatga tggattatct ataatatctg 550
ttatagtaaa tgtttgctac gatttctctt tgaacaattt gtcaatatcg 600
ccttacatat gtggaggagc aggggtagat gctatagaat tcttcgatgt 650
attacacatt aagtttgc atcaaagcaa gctaggtatt gcttattctc 700
taccatctaa cattagtctc ttgctagtt tatattacca taaagtaatg 750
ggcaatcaat ttaaaaattt aaatgtccaa catgttgctg aacttgcaag 800
tatacctaaa attacatccg cagttgctac acttaatat gggtattttg 850
gaggtgaaat tggtgcaaga ttgacattt 879

<210> 40

<211> 293

<212> PRT

<213> *Ehrlichia canis*

<220>

<223> amino acid sequence of *E. canis* p28-1 protein

<400> 40

Met	Asn	Asn	Lys	Leu	Lys	Phe	Thr	Ile	Ile	Asn	Thr	Val	Leu	Val
			5						10					15
Cys	Leu	Leu	Ser	Leu	Pro	Asn	Ile	Ser	Ser	Ser	Lys	Ala	Ile	Asn
			20						25					30
Asn	Asn	Ala	Lys	Lys	Tyr	Tyr	Gly	Leu	Tyr	Ile	Ser	Gly	Gln	Tyr
			35						40					45
Lys	Pro	Ser	Val	Ser	Val	Phe	Ser	Asn	Phe	Ser	Val	Lys	Glu	Thr
			50						55					60
Asn	Val	Ile	Thr	Lys	Asn	Leu	Ile	Ala	Leu	Lys	Lys	Asp	Val	Asp
			65						70					75
Ser	Ile	Glu	Thr	Lys	Thr	Asp	Ala	Ser	Val	Gly	Ile	Ser	Asn	Pro
			80						85					90
Ser	Asn	Phe	Thr	Ile	Pro	Tyr	Thr	Ala	Val	Phe	Gln	Asp	Asn	Ser
			95						100					105
Val	Asn	Phe	Asn	Gly	Thr	Ile	Gly	Tyr	Thr	Phe	Ala	Glu	Gly	Thr
			110						115					120
Arg	Val	Glu	Ile	Glu	Gly	Ser	Tyr	Glu	Glu	Phe	Asp	Val	Lys	Asn
			125						130					135
Pro	Gly	Gly	Tyr	Thr	Leu	Ser	Asp	Ala	Tyr	Arg	Tyr	Phe	Ala	Leu
			140						145					150
Ala	Arg	Glu	Met	Lys	Gly	Asn	Ser	Phe	Thr	Pro	Lys	Glu	Lys	Val
			155						160					165
Ser	Asn	Ser	Ile	Phe	His	Thr	Val	Met	Arg	Asn	Asp	Gly	Leu	Ser
			170						175					180
Ile	Ile	Ser	Val	Ile	Val	Asn	Val	Cys	Tyr	Asp	Phe	Ser	Leu	Asn
			185						190					195
Asn	Leu	Ser	Ile	Ser	Pro	Tyr	Ile	Cys	Gly	Gly	Ala	Gly	Val	Asp
			200						205					210
Ala	Ile	Glu	Phe	Phe	Asp	Val	Leu	His	Ile	Lys	Phe	Ala	Tyr	Gln
			215						220					225
Ser	Lys	Leu	Gly	Ile	Ala	Tyr	Ser	Leu	Pro	Ser	Asn	Ile	Ser	Leu
			230						235					240

Phe	Ala	Ser	Leu	Tyr	Tyr	His	Lys	Val	Met	Gly	Asn	Gln	Phe	Lys
				245					250					255
Asn	Leu	Asn	Val	Gln	His	Val	Ala	Glu	Leu	Ala	Ser	Ile	Pro	Lys
				260					265					270
Ile	Thr	Ser	Ala	Val	Ala	Thr	Leu	Asn	Ile	Gly	Tyr	Phe	Gly	Gly
				275					280					285
Glu	Ile	Gly	Ala	Arg	Leu	Thr	Phe							
				290			293							

<210> 41

<211> 840

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of *E. canis* p28-2

<400> 41

atgaattata	agaaaattct	agtaagaagc	gcgttaatct	cattaatgtc	50
aatcttacca	tatcagtctt	ttgcagatcc	tgtagggttca	agaactaatg	100
ataacaaaga	aggcttctac	attagtgcaa	agtacaatcc	aagtatatca	150
cacttttagaa	aattctctgc	tgaagaaact	cctattaatg	gaacaaattc	200
tctcactaaa	aaagttttcg	gactaaagaa	agatggtgat	ataacaaaaa	250
aagacgattt	tacaagagta	gctccaggca	ttgatttttca	aaataactta	300
atatcaggat	tttcaggaag	tattgggttac	tctatggacg	gaccaagaat	350
agaacttgaa	gctgcatatc	aacaatttaa	tccaaaaaac	accgataaca	400
atgatactga	taatggtgaa	tactataaac	atthttgcatt	atctcgtaaa	450
gatgcaatgg	aagatcagca	atatgtagta	cttaaaaaatg	acggcataac	500
ttttatgtca	ttgatggtta	atacttgcta	tgacattaca	gctgaaggag	550
tatcttttcgt	accatatgca	tgtgcaggta	taggagcaga	tcttatcact	600
atthtttaaag	acctcaatct	aaaatttgct	taccaaggaa	aaataggtat	650
tagttaccct	atcacaccag	aagtctctgc	atttattggt	ggatactacc	700
atggcgttat	tggttaataaa	tttgagaaga	tacctgtaat	aactcctgta	750
gtattaaatg	atgctcctca	aaccacatct	gcttcagtaa	ctcttgacgt	800
tggatacttt	ggcggagaaa	ttggaatgag	gttcaccttc		840

<210> 42
 <211> 280
 <212> PRT
 <213> *Ehrlichia canis*

 <220>
 <223> amino acid sequence of *E. canis* p28-2 protein

<400> 42
 Met Asn Tyr Lys Lys Ile Leu Val Arg Ser Ala Leu Ile Ser Leu
 5 10 15
 Met Ser Ile Leu Pro Tyr Gln Ser Phe Ala Asp Pro Val Gly Ser
 20 25 30
 Arg Thr Asn Asp Asn Lys Glu Gly Phe Tyr Ile Ser Ala Lys Tyr
 35 40 45
 Asn Pro Ser Ile Ser His Phe Arg Lys Phe Ser Ala Glu Glu Thr
 50 55 60
 Pro Ile Asn Gly Thr Asn Ser Leu Thr Lys Lys Val Phe Gly Leu
 65 70 75
 Lys Lys Asp Gly Asp Ile Thr Lys Lys Asp Asp Phe Thr Arg Val
 80 85 90
 Ala Pro Gly Ile Asp Phe Gln Asn Asn Leu Ile Ser Gly Phe Ser
 95 100 105
 Gly Ser Ile Gly Tyr Ser Met Asp Gly Pro Arg Ile Glu Leu Glu
 110 115 120
 Ala Ala Tyr Gln Gln Phe Asn Pro Lys Asn Thr Asp Asn Asn Asp
 125 130 135
 Thr Asp Asn Gly Glu Tyr Tyr Lys His Phe Ala Leu Ser Arg Lys
 140 145 150
 Asp Ala Met Glu Asp Gln Gln Tyr Val Val Leu Lys Asn Asp Gly
 155 160 165
 Ile Thr Phe Met Ser Leu Met Val Asn Thr Cys Tyr Asp Ile Thr
 170 175 180
 Ala Glu Gly Val Ser Phe Val Pro Tyr Ala Cys Ala Gly Ile Gly
 185 190 195

Ala	Asp	Leu	Ile	Thr	Ile	Phe	Lys	Asp	Leu	Asn	Leu	Lys	Phe	Ala
				200					205					210
Tyr	Gln	Gly	Lys	Ile	Gly	Ile	Ser	Tyr	Pro	Ile	Thr	Pro	Glu	Val
				215					220					225
Ser	Ala	Phe	Ile	Gly	Gly	Tyr	Tyr	His	Gly	Val	Ile	Gly	Asn	Lys
				230					235					240
Phe	Glu	Lys	Ile	Pro	Val	Ile	Thr	Pro	Val	Val	Leu	Asn	Asp	Ala
				245					250					255
Pro	Gln	Thr	Thr	Ser	Ala	Ser	Val	Thr	Leu	Asp	Val	Gly	Tyr	Phe
				260					265					270
Gly	Gly	Glu	Ile	Gly	Met	Arg	Phe	Thr	Phe					
				275					280					

<210> 43
 <211> 828
 <212> DNA
 <213> *Ehrlichia canis*

<220>
 <223> nucleic acid sequence of *E. canis* p28-3

<400> 43
 atgaactgta aaaaaattct tataacaact acattggtat cactaacaat 50
 tctttttacct ggcataatctt tctccaaacc aatacatgaa aacaatacta 100
 caggaaactt ttacattatt ggaaaatatg taccaagtat ttcacatttt 150
 gggaactttt cagctaaaga agaaaaaac acaacaactg gaatttttgg 200
 attaaaagaa tcatggactg gtggtatcat ccttgataaa gaacatgcag 250
 cttttaatat cccaaattat tcatttaaata atgaaaataa tccattttta 300
 ggatttgcag gggtaattgg ctattcaata ggtagtccaa gaatagaatt 350
 tgaagtatca tacgagacat tcgatgtaca aaatccagga gataagttta 400
 acaatgatgc acataagtat tgtgctttat ccaatgattc cagtaaaaca 450
 atgaaaagtg gtaaattcgt ttttctcaaa aatgaaggat taagtgcacat 500
 atcactcatg ttaaattgtat gttatgatat aataaacaaa agaatgcctt 550
 tttcacctta catatgtgca ggcattggta ctgacttaat attcatgttt 600
 gacgctataa accataaagc tgcttatcaa ggaaaattag gttttaatta 650

tccaataagc ccagaagcta acatttctat ggggtgtgcac tttcacaaag 700
 taacaaacaa cgagttttaga gttcctgttc tattaactgc tggaggactc 750
 gctccagata atctatttgc aatagtaaag ttgagtatat gtcatttttg 800
 gttagaattt ggggtacaggg tcagtttt 828

<210> 44

<211> 276

<212> PRT

<213> *Ehrlichia canis*

<220>

<223> amino acid sequence of *E. canis* p28-3 protein

<400> 44

Met	Asn	Cys	Lys	Lys	Ile	Leu	Ile	Thr	Thr	Thr	Leu	Val	Ser	Leu	5	10	15
Thr	Ile	Leu	Leu	Pro	Gly	Ile	Ser	Phe	Ser	Lys	Pro	Ile	His	Glu	20	25	30
Asn	Asn	Thr	Thr	Gly	Asn	Phe	Tyr	Ile	Ile	Gly	Lys	Tyr	Val	Pro	35	40	45
Ser	Ile	Ser	His	Phe	Gly	Asn	Phe	Ser	Ala	Lys	Glu	Glu	Lys	Asn	50	55	60
Thr	Thr	Thr	Gly	Ile	Phe	Gly	Leu	Lys	Glu	Ser	Trp	Thr	Gly	Gly	65	70	75
Ile	Ile	Leu	Asp	Lys	Glu	His	Ala	Ala	Phe	Asn	Ile	Pro	Asn	Tyr	80	85	90
Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Val	95	100	105
Ile	Gly	Tyr	Ser	Ile	Gly	Ser	Pro	Arg	Ile	Glu	Phe	Glu	Val	Ser	110	115	120
Tyr	Glu	Thr	Phe	Asp	Val	Gln	Asn	Pro	Gly	Asp	Lys	Phe	Asn	Asn	125	130	135
Asp	Ala	His	Lys	Tyr	Cys	Ala	Leu	Ser	Asn	Asp	Ser	Ser	Lys	Thr	140	145	150

Met	Lys	Ser	Gly	Lys	Phe	Val	Phe	Leu	Lys	Asn	Glu	Gly	Leu	Ser	155	160	165
Asp	Ile	Ser	Leu	Met	Leu	Asn	Val	Cys	Tyr	Asp	Ile	Ile	Asn	Lys	170	175	180
Arg	Met	Pro	Phe	Ser	Pro	Tyr	Ile	Cys	Ala	Gly	Ile	Gly	Thr	Asp	185	190	195
Leu	Ile	Phe	Met	Phe	Asp	Ala	Ile	Asn	His	Lys	Ala	Ala	Tyr	Gln	200	205	210
Gly	Lys	Leu	Gly	Phe	Asn	Tyr	Pro	Ile	Ser	Pro	Glu	Ala	Asn	Ile	215	220	225
Ser	Met	Gly	Val	His	Phe	His	Lys	Val	Thr	Asn	Asn	Glu	Phe	Arg	230	235	240
Val	Pro	Val	Leu	Leu	Thr	Ala	Gly	Gly	Leu	Ala	Pro	Asp	Asn	Leu	245	250	255
Phe	Ala	Ile	Val	Lys	Leu	Ser	Ile	Cys	His	Phe	Gly	Leu	Glu	Phe	260	265	270
Gly	Tyr	Arg	Val	Ser	Phe										275		

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 <213> *Ehrlichia canis*

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 <223> nucleic acid sequence of *E. canis* p28-9

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 aatttttcag ctgaagaaac aattcctggt attacaaaaa agatttttgc 200
 gttaggtcctt gataagtctg agataaatac tcacagcaat ttacacgat 250
 catatgaccc tacttatgca agcagttttg cagggttttag tggtatcatt 300
 ggatattatg ttaatgactt tagggtagaa tttgaagggtt cttatgagaa 350


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<220>
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Val Phe Phe Leu Ser Asp Gly Ala Phe Ser Asp Ala Asn Phe Ser
          20                      25                      30
Glu Gly Arg Arg Gly Leu Tyr Ile Gly Ser Gln Tyr Lys Val Gly
          35                      40                      45
Ile Pro Asn Phe Ser Asn Phe Ser Ala Glu Glu Thr Ile Pro Gly
          50                      55                      60
Ile Thr Lys Lys Ile Phe Ala Leu Gly Leu Asp Lys Ser Glu Ile
          65                      70                      75
Asn Thr His Ser Asn Phe Thr Arg Ser Tyr Asp Pro Thr Tyr Ala
          80                      85                      90
Ser Ser Phe Ala Gly Phe Ser Gly Ile Ile Gly Tyr Tyr Val Asn
          95                      100                     105

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Asp	Phe	Arg	Val	Glu	Phe	Glu	Gly	Ser	Tyr	Glu	Asn	Phe	Glu	Pro
				110					115					120
Glu	Arg	Gln	Trp	Tyr	Pro	Glu	Asn	Ser	Gln	Ser	Tyr	Lys	Phe	Phe
				125					130					135
Ala	Leu	Ser	Arg	Asn	Ala	Thr	Asn	Ser	Asp	Asn	Lys	Phe	Ile	Val
				140					145					150
Leu	Glu	Asn	Asn	Gly	Val	Val	Asp	Lys	Ser	Leu	Asn	Val	Asn	Val
				155					160					165
Cys	Tyr	Asp	Ile	Ala	Ser	Gly	Ser	Ile	Pro	Leu	Ala	Pro	Tyr	Met
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Cys	Ala	Gly	Val	Gly	Ala	Asp	Tyr	Ile	Lys	Phe	Leu	Gly	Ile	Ser
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Leu	Pro	Lys	Phe	Ser	Tyr	Gln	Val	Lys	Phe	Gly	Val	Asn	Tyr	Pro
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Leu	Asn	Val	Asn	Thr	Met	Leu	Phe	Gly	Gly	Gly	Tyr	Tyr	His	Lys
				215					220					225
Val	Val	Gly	Asp	Arg	His	Glu	Arg	Val	Glu	Ile	Ala	Tyr	His	Pro
				230					235					240
Thr	Ala	Leu	Ser	Asp	Val	Pro	Arg	Thr	Thr	Ser	Ala	Ser	Ala	Thr
				245					250					255
Leu	Asn	Thr	Asp	Tyr	Phe	Gly	Trp	Glu	Ile	Gly	Phe	Arg	Phe	Ala
				260					265					270
Leu														
271														